

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/480,977DATE: 03/17/2000
TIME: 02:47:09

INPUT SET: S35068.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

- 1
2
3 (1) General Information:
4
5 (i) APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
6
7 (ii) TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
8 Ligands and Uses Therefor
9
10 (iii) NUMBER OF SEQUENCES: 23
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Genentech, Inc.
14 (B) STREET: 1 DNA Way
15 (C) CITY: South San Francisco
16 (D) STATE: California
17 (E) COUNTRY: USA
18 (F) ZIP: 94080
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: WinPatin (Genentech)
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER: 09/480,977
28 (B) FILING DATE:
29 (C) CLASSIFICATION:
30
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: 08/899,437
33 (B) FILING DATE: 24-Jul-1997
34
35 (viii) ATTORNEY/AGENT INFORMATION:
36 (A) NAME: Conley, Deirdre L.
37 (B) REGISTRATION NUMBER: 36,487
38 (C) REFERENCE/DOCKET NUMBER: P1084R1
39
40 (ix) TELECOMMUNICATION INFORMATION:
41 (A) TELEPHONE: 650/225-2066
42 (B) TELEFAX: 650/952-9881
43 (2) INFORMATION FOR SEQ ID NO:1:
44
45 (i) SEQUENCE CHARACTERISTICS:
46 (A) LENGTH: 2538 base pairs

ENTERED

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nH
5-5-00

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47 (B) TYPE: Nucleic Acid
48 (C) STRANDEDNESS: Single
49 (D) TOPOLOGY: Linear
50

51 (ix) FEATURE:
52 (A) NAME/KEY: mouse NRG3 nucleic acid
53 (B) LOCATION: 1-2538
54 (C) IDENTIFICATION METHOD:
55 (D) OTHER INFORMATION:
56

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58
59

60 CCTGACCGGC CGGCGGCGCC CGGGCCGGTC TCGCCCCTCT ACCGAGCGCC 50
61
62 TCGCCGCCCC CTCCCCGGCC CGCGTCCCCT CCCCCGTCCT CTCCTCCCCG 100
63
64 CCCGCCGCCC GCCTCTCGGG GGGAGGGGCG TGGGGGCAGG GAGCCGATTT 150
65
66 GCATGCGGCC GCCGCGGCCG CTGCCTGAGC CGGAGCCCGC CGCCGCCGGA 200
67
68 GCCCGCGCCC GCGCCCGCGC CCGGCCCGCG CGGCCCATG CCTCTGGCGC 250
69
70 GGCCCTCGGG GGGGCGAAGG TGAAGATCGG CTCCTAGGAT GAGTGAAGGG 300
71
72 GCGGCCGGTG CCTCGCCACC TGGTGCCGCT TCGGCAGCCG CCGCCTCAGC 350
73
74 CGAGGAGGGC ACCGCGGCGG CTGCGGCGGC GGCGGCGGCG GGCGGGGGCC 400
75
76 CGGACGGCGG CGGAGAAGGG GCGGCCGAAC CCCCCCGGGA GTTACGCTGT 450
77
78 AGCGACTGCA TCGTGTGGAA CCGGCAGCAG ACGTGGTTGT GCGTGGTGCC 500
79
80 TCTGTTCATC GGCTTCATCG GCCTGGGGCT CAGCCTCATG CTGCTTAAAT 550
81
82 GGATCGTGGT AGGCTCCGTC AAGGAGTACG TGCCACGGA CCTGGTGGAC 600
83
84 TCCAAGGGAA TGGGCCAGGA CCCCTTCTTC CTCTCCAAGC CCAGCTCTTT 650
85
86 CCCCAAGGCT ATGGAAACCA CCACAACAAC CACTTCTACC ACGTCCCCCG 700
87
88 CCACCCCCTC TGCCGGCGGC GCCGCTTCTT CCAGGACGCC TAACCGGATT 750
89
90 AGCACCCGCT TGACCACCAT CACACGGGCA CCCACCCGCT TCCCTGGGCA 800
91
92 CCGGGTTCCC ATCCGGGCTA GCCCGCGCTC TACCACAGCA CGGAACACTG 850
93
94 CTGCCCCCTC GACGGTCCTG TCCACCACGG CCCCTTCTT CAGTAGCAGC 900
95
96 ACGCCCGGCT CCCGACCCC GATGCCAGGA GCCCCAGTA CGCAGGCGAT 950
97
98 GCCTTCCTGG CCCACTGCGG CGTATGCTAC CTCCTCCTAC CTCCACGATT 1000
99

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100 CCACTCCCTC CTGGACCCTG TCACCCTTTC AGGATGCTGC TGCCGCCTCT 1050
101
102 TCCTCCTCAC CCTCTTCCAC CTCCTCCACT ACCACCACCC CAGAAACTAG 1100
103
104 CACCAGCCCC AAATTTTCATA CTACAACATA CTCCACTGAA CGATCTGAGC 1150
105
106 ACTTCAAACC CTGTCGAGAC AAGGACCTGG CGTATTGTCT CAATGATGGT 1200
107
108 GAATGCTTTG TGATTGAGAC CCTGACAGGA TCCCATAAGC ACTGTCGGTG 1250
109
110 CAAGGAAGGC TACCAAGGAG TCCGTTGTGA TCAATTTCTG CCGAAAACAG 1300
111
112 ACTCCATCTT ATCGGATCCA ACAGACCACT TGGGGATTGA ATTCATGGAG 1350
113
114 AGTGAAGACG TTTATCAAAG GCAGGTGCTG TCAATTTTCAT GTATCATCTT 1400
115
116 TGGAATTGTC ATCGTGGGCA TGTCTGTGC AGCATTCTAC TTCAAAGCA 1450
117
118 AGAAACAAGC TAAACAAATT CAGGAGCACC TGAAAGAGTC ACAGAATGGG 1500
119
120 AAGAACTACA GCCTCAAGGC ATCCAGCACA AAGTCTGAGA GCTTGATGAA 1550
121
122 GAGCCATGTC CATCTACAAA ATTATTCAAA GGCGGATAGG CATCCTGTGA 1600
123
124 CTGCGCTGGA GAAAATAATG GAGTCAAGTT TTTCAGCTCC CCAGTCGTTC 1650
125
126 CCAGAAGTCA CTTCTCCTGA CCGAGGAAGC CAGCCTATCA AGCACCACAG 1700
127
128 CCCAGGACAA AGGAGTGGGA TGTTGCATAG GAATACTTTC AGAAGGGCAC 1750
129
130 CACCCTCACC CCGAAGTCGA CTGGGTGGTA TTGTAGGACC AGCATATCAA 1800
131
132 CAACTTGAAG AATCAAGAAT TCCAGACCAG GATACGATAC CTTGCCAAGG 1850
133
134 GATAGAGGTC AGGAAGACTA TATCCCACCT GCCTATACAG CTGTGGTGTG 1900
135
136 TTGAAAGACC CCTGGACTTA AAGTATGTGT CCAATGGCTT AAGAACCCAA 1950
137
138 CAAAATGCAT CAATAAATAT GCAACTGCCT TCAAGAGAGA CAAACCCCTA 2000
139
140 TTTTAATAGC TTGGATCAAA AGGACCTGGT GGGTTATTTA TCCCAAGGG 2050
141
142 CCAATTCTGT GCCCATCATC CCGTCGATGG GTCTAGAAGA AACCTGCATG 2100
143
144 CAAATGCCAG GGATTTCTGA CGTCAAAGC ATTAAATGGT GCAAAAACCTC 2150
145
146 CTACTCCGCT GACATTGTCA ACGCGAGTAT GCCAGTCAGT GATTGTCTTC 2200
147
148 TAGAAGAACA ACAGGAAGTG AAAATATTAC TAGAGACTGT GCAGGAACAG 2250
149
150 ATCCGGATTG TGAATGATGC CAGACGGTCA GAAGACTTCG AACTGGCCAG 2300
151
152 CATGGAACT GAGGACAGTG CGAGCGAAAA CACAGCCTTT CTCCCCCTGA 2350

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153
154 GTCCACGGC CAAATCAGAA CGAGAGGCAC AATTTGTCTT AAGAAATGAA 2400
155
156 ATACAAAGAG ACTCTGTGCT AACCAAGTGA CTGGAAATGT AGGAATCTGT 2450
157
158 GCATTATATG CTTTGCTAAA CAGGAAGGAG AGGAAATTAA ATACAAATTA 2500
159
160 TTTATATGCA TTAATTTAAG AGCATCTACT TAGAAGCC 2538
161
162 (2) INFORMATION FOR SEQ ID NO:2:
163
164 (i) SEQUENCE CHARACTERISTICS:
165 (A) LENGTH: 713 amino acids
166 (B) TYPE: Amino Acid
167 (D) TOPOLOGY: Linear
168
169 (ix) FEATURE:
170 (A) NAME/KEY: Mouse NRG3 (mNRG3)/amino acid seq.
171 (B) LOCATION: 1-713
172 (C) IDENTIFICATION METHOD:
173 (D) OTHER INFORMATION:
174
175 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
176
177 Met Ser Glu Gly Ala Ala Gly Ala Ser Pro Pro Gly Ala Ala Ser
178 1 5 10 15
179
180 Ala Ala Ala Ala Ser Ala Glu Glu Gly Thr Ala Ala Ala Ala Ala
181 20 25 30
182
183 Ala Ala Ala Ala Gly Gly Gly Pro Asp Gly Gly Gly Glu Gly Ala
184 35 40 45
185
186 Ala Glu Pro Pro Arg Glu Leu Arg Cys Ser Asp Cys Ile Val Trp
187 50 55 60
188
189 Asn Arg Gln Gln Thr Trp Leu Cys Val Val Pro Leu Phe Ile Gly
190 65 70 75
191
192 Phe Ile Gly Leu Gly Leu Ser Leu Met Leu Leu Lys Trp Ile Val
193 80 85 90
194
195 Val Gly Ser Val Lys Glu Tyr Val Pro Thr Asp Leu Val Asp Ser
196 95 100 105
197
198 Lys Gly Met Gly Gln Asp Pro Phe Phe Leu Ser Lys Pro Ser Ser
199 110 115 120
200
201 Phe Pro Lys Ala Met Glu Thr Thr Thr Thr Thr Thr Ser Thr Thr
202 125 130 135
203
204 Ser Pro Ala Thr Pro Ser Ala Gly Gly Ala Ala Ser Ser Arg Thr
205 140 145 150

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206
207   Pro Asn Arg Ile Ser Thr Arg Leu Thr Thr Ile Thr Arg Ala Pro
208                               155                               160                               165
209
210   Thr Arg Phe Pro Gly His Arg Val Pro Ile Arg Ala Ser Pro Arg
211                               170                               175                               180
212
213   Ser Thr Thr Ala Arg Asn Thr Ala Ala Pro Pro Thr Val Leu Ser
214                               185                               190                               195
215
216   Thr Thr Ala Pro Phe Phe Ser Ser Ser Thr Pro Gly Ser Arg Pro
217                               200                               205                               210
218
219   Pro Met Pro Gly Ala Pro Ser Thr Gln Ala Met Pro Ser Trp Pro
220                               215                               220                               225
221
222   Thr Ala Ala Tyr Ala Thr Ser Ser Tyr Leu His Asp Ser Thr Pro
223                               230                               235                               240
224
225   Ser Trp Thr Leu Ser Pro Phe Gln Asp Ala Ala Ala Ala Ser Ser
226                               245                               250                               255
227
228   Ser Ser Pro Ser Ser Thr Ser Ser Thr Thr Thr Thr Pro Glu Thr
229                               260                               265                               270
230
231   Ser Thr Ser Pro Lys Phe His Thr Thr Thr Tyr Ser Thr Glu Arg
232                               275                               280                               285
233
234   Ser Glu His Phe Lys Pro Cys Arg Asp Lys Asp Leu Ala Tyr Cys
235                               290                               295                               300
236
237   Leu Asn Asp Gly Glu Cys Phe Val Ile Glu Thr Leu Thr Gly Ser
238                               305                               310                               315
239
240   His Lys His Cys Arg Cys Lys Glu Gly Tyr Gln Gly Val Arg Cys
241                               320                               325                               330
242
243   Asp Gln Phe Leu Pro Lys Thr Asp Ser Ile Leu Ser Asp Pro Thr
244                               335                               340                               345
245
246   Asp His Leu Gly Ile Glu Phe Met Glu Ser Glu Asp Val Tyr Gln
247                               350                               355                               360
248
249   Arg Gln Val Leu Ser Ile Ser Cys Ile Ile Phe Gly Ile Val Ile
250                               365                               370                               375
25

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252	Val Gly Met Phe Cys Ala Ala Phe Tyr Phe Lys Ser Lys Lys Gln	
253		380 385 390
254		
255	Ala Lys Gln Ile Gln Glu His Leu Lys Glu Ser Gln Asn Gly Lys	
256		395 400 405
257		
258	Asn Tyr Ser Leu Lys Ala Ser Ser Thr Lys Ser Glu Ser Leu Met	

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SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text

PAGE: 1

SEQUENCE MISSING ITEM REPORT
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< < THERE ARE NO ITEMS MISSING > >

PAGE: 1

SEQUENCE CORRECTION REPORT
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INPUT SET: S35068.raw

Line	Original Text	Corrected Text
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